



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/729,340B
Source: IFWO
Date Processed by STIC: 10/28/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE~~ ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebs/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/729,340B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- found globally*
- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
 - 2 ☒ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
 - 3 ☐ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
 - 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
 - 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
 - 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
 - 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
 - 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
 - 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
 - 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
 - 11 ☐ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
 - 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
 - 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 10/28/2004

PATENT APPLICATION: US/10/729,340B

TIME: 15:43:45

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\10282004\J729340B.raw

1 <110> APPLICANT: Jager, Dirk
 2 Stockert, Elizabeth
 3 Scanlan, Matthew
 4 Gure, Ali
 5 Knuth, Alexander
 6 Old, Lloyd
 7 Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,

*see item 2 on Euro
summary sheet*

10 the Antigens Per Se, and Uses Thereof
 12 <130> FILE REFERENCE: LUD 5793.1
 14 <140> CURRENT APPLICATION NUMBER: US 10/729,340B
 15 <141> CURRENT FILING DATE: 2003-12-04
 17 <150> PRIOR APPLICATION NUMBER: US 60/430,869
 18 <151> PRIOR FILING DATE: 2002-12-04
 20 <150> PRIOR APPLICATION NUMBER: US 10/181,663
 21 <151> PRIOR FILING DATE: 2000-11-29
 23 <150> PRIOR APPLICATION NUMBER: US 09/602,362
 24 <151> PRIOR FILING DATE: 2000-06-22
 26 <150> PRIOR APPLICATION NUMBER: US 09/451,739
 27 <151> PRIOR FILING DATE: 1999-11-30
 29 <160> NUMBER OF SEQ ID NOS: 32
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1533
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens

**Does Not Comply
Corrected Diskette Needed**

W--> 35 <220> FEATURE:

36 <221> NAME/KEY: CDS

37 <222> LOCATION: 235

W--> 38 <400> SEQUENCE: 1

39 gggtttccac gttggacaag tgcggctcgg cggccagcgg agcgcgcccc ttcccgtgc 60
 40 ccgctccgct cctctcttct acccagccca gtggcgaggt gggcagcggc ggccgcggcg 120
 41 ctggggccctc tccgcgggt gtgtgcgcgc tcgtacgcgc ggccccggc gccagccccg 180
 W--> 42 ccgcctgaga gggggcctgc gccgcgggcc ggggcgtgcg cccgggagcc accgncaccg 240
 43 cggcccgcgc cctcaggcgc tggggctccc gcggaccgcg aggcggcgga cgggctcggc 300
 44 agatgtagcc gccggggcga agcaggagcc ggcggggggg cgccgggaga gcgaggcgtt 360
 45 tgcattttgc agtgctattt tttgaggggg gcggaggggt gaggaagtcg gaaagccgcg 420
 46 ccgagtcgcc ggggacctcc ggggtgaacc atgttgagtc ctgccaacgg ggagcagctc 480
 47 cacctggtga actatgtgga ggactacctg gactccatcg agtccctgcc tttcgacttg 540
 48 cagagaaatg tctcgctgat gcgggagatc gacgcgaaat accaagagat cctgaaggag 600
 49 ctgacgaggt gctacgagcg cttcagtcgc gagacagacg gggcgagaa gcggcgagatg 660
 50 ctgcactgtg tgcagcgcgc gctgatccgc agccaggagc tgggcgacga gaagatccag 720
 51 atcgtgagcc agatggtgga gctggtggag aaccgcacgc ggcaggtgga cagccacgtg 780
 52 gagctgttcg aggcgcagca ggagctgggc gacacagcgg gcaacagcgg caaggtcggc 840

*this does not explain "n" at location 235
(see p.7 for euro
explanation)*

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Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\10282004\J729340B.raw

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53 gcggacagggc ccaaaggcga ggcggcagcg caggctgaca agcccaacag caagcgctca 900
54 cggcggcagc gcaacaacga gaaccgtgag aacgcgtcca gcaaccacga ccacgacgac 960
55 ggcgcctcgg gcacacccaa ggagaagaag gccaaagacct ccaagaagaa gaagcgctcc 1020
56 aaggccaagg cggagcgaga ggcgtccct gccagacct ccacgaccc caacgaaccc 1080
57 acgtactgtc tgtgcaacca ggtctcctat ggggagatga tcggctgcga caacgacgag 1140
58 tgcccatcg agtgggttcca cttctcgtgc gtggggctca atcataaacc caagggcaag 1200
59 tggtagctgc ccaagtgcg ggggggagaac gagaagacca tggacaaagc cctggagaaa 1260
60 tccaaaaaag agagggctta caacaggtag tttgtggaca ggcgcctggg gtgaggagga 1320
61 caaaataaac cgtgtattta ttacattgct gcctttgttg aggtgcaagg agtgtaaaat 1380
62 gtatatTTTT aaagaatggt agaaaaggaa ccattccttt catagggatg gcagtgatTC 1440
63 tgtttgcctt ttgttttcat tggtagacgt gtaacaagaa agtgggtctgt ggatcagcat 1500
64 tttagaaact acaaatatag gtttgattca aca 1533

```

67 <210> SEQ ID NO: 2

68 <211> LENGTH: 1143

69 <212> TYPE: DNA

70 <213> ORGANISM: Homo sapiens

W--> 71 <400> SEQUENCE: 2

```

72 gagtaaccgg ataatatgcc gttgtccggc acggcgacga gaattcccag atatagcagt 60
73 agcagtgate ccgggctgt ggtcggggc cggggctgca gttcggaccg cctcccgcga 120
74 cccgcggggc ctccgagaca gtttcaggcc gcattcttgc tgacccgagg gtggggccgc 180
75 gcgtggcgt ggaacagat cctgaaggag ctagacgagt gctacgagcg cttcagtcgc 240
76 gagacagacg gggcgagaa ggcgcggatg ctgcactgtg tgcagcgcg gctgatccgc 300
77 agccaggagc tggcgacga gaagatccag atcgtgagcc agatgggtga gctgggtgag 360
78 aaccgcagcg ggcagggtga cagccacgtg gagctgttcg aggcgcagca ggagctgggc 420
79 gacacagtgg gcaacagcgg caaggttggc gcggacaggg ccaatggcga tgcggtagcg 480
80 cagtctgaca agcccaacag caagcgctca cggcggcagc gcaacaacga gaaccgtgag 540
81 aacgcgtcca gcaaccacga ccacgacgac ggcgcctcgg gcacacccaa ggagaagaag 600
82 gccaaagacct ccaagaagaa gaagcgctcc aaggccaagg cggagcgaga ggcgtccct 660
83 gccgacctcc ccacgaccc caacgaaccc acgtactgtc tgtgcaacca ggtctcctat 720
84 ggggagatga tcggctgcga caacgacgag tgcccatcg agtgggttcca cttctcgtgc 780
85 gtggggctca atcataaacc caagggcaag tggtagctgc ccaagtgcg gggggagaac 840
86 gagaagacca tggacaaagc cctggagaaa tccaaaaaag agagggctta caacaggtag 900
87 tttgtggaca ggcgcctggg gtgaggagga caaaataaac cgtgtattta ttacattgct 960
88 gcctttgttg aggtgcaagg agtgtaaaat gtatatTTTT aaagaatggt agaaaaggaa 1020
89 ccattccttt catagggatg gcagtgatTC tgtttgcctt ttgttttcat tggtagacgt 1080
90 gtaacaagaa agtgggtctgt ggatcagcat tttagaaact acaaatatag gtttgattca 1140
91 aca 1143

```

94 <210> SEQ ID NO: 3

95 <211> LENGTH: 742

96 <212> TYPE: DNA

97 <213> ORGANISM: Homo sapiens

W--> 98 <400> SEQUENCE: 3

```

99 cgccgtccac acccagcgg cctgacgt gtccctcccg cgaccctcgc ctctggaaaa 60
100 agtgacaggc aaggccacgc ccccgcgagg gccggcctcg agcccgacg ccccgaggcc 120
101 tgggacgaga tcctgaagga gctagacgag tgctacgagc gcttcagtcg cgagacagac 180
102 ggggcgagc agaagatcca gatcgtgagc cagatggtgg agctgggtga gaaccgcagc 240
103 ctgggagcag agaagatcca gatcgtgagc cagatggtgg agctgggtga gaaccgcagc 300
104 cggcagggtg acagccacgt ggagctgttc gaggcgcagc aggagctggg cgacacagcg 360
105 ggcaacagcg gcaaggctgg cgcggacagg cccaaaggcg aggcgcgagc gcaggctgac 420

```

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TIME: 15:43:45

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\10282004\J729340B.raw

```

106 aagcccaaca gcaagcgctc acggcggcag cgcaacaacg agaaccgtga gaacgcgtcc 480
107 agcaaccacg accacgacga cggcgccctcg ggcacaccca aggagaagaa ggccaagacc 540
108 tccaagaaga agaagcgctc caaggccaag gcggagcgag aggcgtcccc tgccgacctc 600
109 cccatcgacc ccaacgaacc cagtgactgt ctgtgcaacc aggtctccta tggggagatg 660
110 atcggtgcg acaacgacga gtgccccatc gagtgggttc acttctcgtg cgtggggctc 720
111 aatcataaac ccaagggcaa gt 742

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114 <210> SEQ ID NO: 4

115 <211> LENGTH: 857

116 <212> TYPE: DNA

117 <213> ORGANISM: Homo sapiens

W--> 118 <400> SEQUENCE: 4

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119 cctccgagaa cgggtgtccat ggcacagggc gggaagagat aaggcctagg gaaggcgccc 60
120 ctcgggccta tccacctctt ctggggctcg gcactaggaa gcagcttccc tctcaggccc 120
121 ctttgtctcc aagccgttcc aaactgagta cgggagacg acacaaaggg agggcggtga 180
122 cggatggcgc aggcgcggga gccgcctagg ctgctgggag tgggtggtcg gccgcggaat 240
123 ggagatcctg aaggagctag acgagtgcta cgagcgcttc agtcgcgaga cagacggggc 300
124 gcagaagcgg cggatgctgc actgtgtgca gcgcgcgctg atccgcagcc aggagctggg 360
125 cgacgagaag atccagatcg tgagccagat ggtggagctg gtggagaacc gcacgcggca 420
126 ggtggacagc cagctggagc tgttcgaggc gcagcaggag ctgggcgaca cagcgggcaa 480
127 cagcggcaag gctggcgcg acaggcccaa aggcgagggc gcagcgcagg ctgacaagcc 540
128 caacagcaag gctcacggc ggcagcgcaa caacgagaac cgtgagaacg cgtccagcaa 600
129 ccacgaccac gacgacggcg cctcgggcac acccaaggag aagaaggcca agacctcaa 660
130 gaagaagaag cgtcccaagg ccaaggcgga gcgagaggcg tccctgccc acctcccat 720
131 cgaccccaac gaaccacgt actgtctgtg caaccaggtc tcctatgggg agatgatcgg 780
132 ctgcgacaac gacgagtgcc ccacgagtg gttccacttc tcgtgcgtgg ggctcaatca 840
133 taaacccaag ggcaagt 857

```

136 <210> SEQ ID NO: 5

137 <211> LENGTH: 279

138 <212> TYPE: PRT

139 <213> ORGANISM: Homo sapiens

W--> 140 <400> SEQUENCE: 5

```

141 Met Leu Ser Pro Ala Asn Gly Glu Gln Leu His Leu Val Asn Tyr Val
142 1 5 10 15
143 Glu Asp Tyr Leu Asp Ser Ile Glu Ser Leu Pro Phe Asp Leu Gln Arg
144 20 25 30
145 Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
146 35 40 45
147 Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
148 50 55 60
149 Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
150 65 70 75 80
151 Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
152 85 90 95
153 Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
154 100 105 110
155 Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys
156 115 120 125
157 Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys
158 130 135 140

```

RAW SEQUENCE LISTING

DATE: 10/28/2004

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TIME: 15:43:45

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\10282004\J729340B.raw

```

159 Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu
160 145 150 155 160
161 Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro
162 165 170 175
163 Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala
164 180 185 190
165 Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn
166 195 200 205
167 Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile
168 210 215 220
169 Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys
170 225 230 235 240
171 Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys
172 245 250 255
173 Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys
174 260 265 270
175 Lys Glu Arg Ala Tyr Asn Arg
176 275

```

179 <210> SEQ ID NO: 6

180 <211> LENGTH: 210

181 <212> TYPE: PRT

182 <213> ORGANISM: Homo sapiens

W--> 183 <400> SEQUENCE: 6

```

184 Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser Gln Glu Leu Gly
185 1 5 10 15
186 Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu Leu Val Glu Asn
187 20 25 30
188 Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe Glu Ala Gln Gln
189 35 40 45
190 Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val Gly Ala Asp Arg
191 50 55 60
192 Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro Asn Ser Lys Arg
193 65 70 75 80
194 Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn Ala Ser Ser Asn
195 85 90 95
196 His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys Glu Lys Lys Ala
197 100 105 110
198 Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys Ala Glu Arg Glu
199 115 120 125
200 Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu Pro Thr Tyr Cys
201 130 135 140
202 Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Asp
203 145 150 155 160
204 Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val Gly Leu Asn His
205 165 170 175
206 Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg Gly Glu Asn Glu
207 180 185 190
208 Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys Glu Arg Ala Tyr
209 195 200 205

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RAW SEQUENCE LISTING

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TIME: 15:43:45

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\10282004\J729340B.raw

210 Asn Arg
 211 210
 214 <210> SEQ ID NO: 7
 215 <211> LENGTH: 235
 216 <212> TYPE: PRT
 217 <213> ORGANISM: Homo sapiens
 W--> 218 <400> SEQUENCE: 7
 219 Met Glu Ile Leu Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg
 220 1 5 10 15
 221 Glu Thr Asp Gly Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg
 222 20 25 30
 223 Ala Leu Ile Arg Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val
 224 35 40 45
 225 Ser Gln Met Val Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser
 226 50 55 60
 227 His Val Glu Leu Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly
 228 65 70 75 80
 229 Asn Ser Gly Lys Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala
 230 85 90 95
 231 Gln Ser Asp Lys Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn
 232 100 105 110
 233 Glu Asn Arg Glu Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala
 234 115 120 125
 235 Ser Gly Thr Pro Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys
 236 130 135 140
 237 Arg Ser Lys Ala Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro
 238 145 150 155 160
 239 Ile Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr
 240 165 170 175
 241 Gly Glu Met Ile Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe
 242 180 185 190
 243 His Phe Ser Cys Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr
 244 195 200 205
 245 Cys Pro Lys Cys Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu
 246 210 215 220
 247 Glu Lys Ser Lys Lys Glu Arg Ala Tyr Asn Arg
 248 225 230 235
 251 <210> SEQ ID NO: 8
 252 <211> LENGTH: 772
 253 <212> TYPE: DNA
 254 <213> ORGANISM: Homo sapiens
 W--> 255 <220> FEATURE:
 256 <221> NAME/KEY: CDS
 257 <222> LOCATION: 695-714
 258 <223> OTHER INFORMATION: n is unknown
 W--> 259 <400> SEQUENCE: 8
 260 aaagcgttct cggcggcagc gcaacaacta gaaccgtgag aacgcgtcca gcaaccgcga 60
 261 cccacgacga cgtcacctcg ggcacgccca aggagaagaa agcccagacc tctaagaaga 120
 262 agcagggtct catggccaag gcgtagcggc aggcgtcccc cgcagacctc cccatcgacc 180

It is at location 689 (see p. 6)

10/729,340B

6

| | | | | | | |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| ccagcgagcc | ctcctactgg | gagatgatcc | gctgcgacaa | cgaatgcccc | atcgagtggg | 240 |
| tccgcttctc | gtgtgtgagt | ctcaaccata | aaccaaagcg | caagtgggtac | tgttccagat | 300 |
| gccggggaaa | gaacgatggg | caaagccctt | gagaagtcca | gaaaaaaaaac | agggcttata | 360 |
| acaggtagtt | tggggacatg | cgtctaatag | tgaggagaaac | aaaataagcc | agtgtgttga | 420 |
| ttacattgcc | acctttgctg | aggtgcagga | agtgtaaaat | gtatatTTTT | aaagaatggt | 480 |
| gtagaggcc | gggcgcgggtg | gctcacgcct | gtaatcccag | cactttggga | ggccgaggcg | 540 |
| gtcggatcac | gaggtcagga | gacgagacc | atcctggcta | acacggtgaa | accccgctctc | 600 |
| tactaaaaat | tcaaaaaaaaa | aattagctgg | gcgtggtggc | gggcgcctgt | agtcccagct | 660 |
| attcgggagg | ctgaggcagg | agaatggc | gaacctggga | ggtggagctt | gcantgagcc | 720 |
| aaggtcgcgc | cactgcactc | cagcctgggc | gacagagcga | gactccatct | ta | 772 |

) location
689

"c" is at
location 695

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/729,340B

DATE: 10/28/2004
TIME: 15:43:46

Input Set : A:\pto.lm.txt
Output Set: N:\CRF4\10282004\J729340B.raw

error explanation

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 235

Seq#:8; N Pos. 689,714

Seq#:15; N Pos. 1628,1752,1758,1769,1789,1873,1908,1915,1933,1970,1976,2022

Seq#:26; N Pos. 439,473,1789

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/729,340B

DATE: 10/28/2004

TIME: 15:43:46

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\10282004\J729340B.raw

L:35 M:283 W: Missing Blank Line separator, <220> field identifier
 L:38 M:283 W: Missing Blank Line separator, <400> field identifier
 L:42 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:1
 L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:180
 L:71 M:283 W: Missing Blank Line separator, <400> field identifier
 L:98 M:283 W: Missing Blank Line separator, <400> field identifier
 L:118 M:283 W: Missing Blank Line separator, <400> field identifier
 L:140 M:283 W: Missing Blank Line separator, <400> field identifier
 L:183 M:283 W: Missing Blank Line separator, <400> field identifier
 L:218 M:283 W: Missing Blank Line separator, <400> field identifier
 L:255 M:283 W: Missing Blank Line separator, <220> field identifier
 L:259 M:283 W: Missing Blank Line separator, <400> field identifier
 L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:660
 L:279 M:283 W: Missing Blank Line separator, <400> field identifier
 L:287 M:283 W: Missing Blank Line separator, <400> field identifier
 L:295 M:283 W: Missing Blank Line separator, <400> field identifier
 L:303 M:283 W: Missing Blank Line separator, <400> field identifier
 L:311 M:283 W: Missing Blank Line separator, <400> field identifier
 L:319 M:283 W: Missing Blank Line separator, <400> field identifier
 L:327 M:283 W: Missing Blank Line separator, <220> field identifier
 L:332 M:283 W: Missing Blank Line separator, <400> field identifier
 L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1620
 L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1740
 L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1860
 L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1920
 L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1980
 L:373 M:283 W: Missing Blank Line separator, <400> field identifier
 L:444 M:283 W: Missing Blank Line separator, <400> field identifier
 L:452 M:283 W: Missing Blank Line separator, <400> field identifier
 L:460 M:283 W: Missing Blank Line separator, <400> field identifier
 L:505 M:283 W: Missing Blank Line separator, <400> field identifier
 L:513 M:283 W: Missing Blank Line separator, <400> field identifier
 L:521 M:283 W: Missing Blank Line separator, <400> field identifier
 L:597 M:283 W: Missing Blank Line separator, <400> field identifier
 L:772 M:283 W: Missing Blank Line separator, <400> field identifier
 L:780 M:283 W: Missing Blank Line separator, <400> field identifier
 L:788 M:283 W: Missing Blank Line separator, <220> field identifier
 L:792 M:283 W: Missing Blank Line separator, <400> field identifier
 L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:420
 L:822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:1740
 L:861 M:283 W: Missing Blank Line separator, <400> field identifier
 L:996 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1004 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1012 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1027 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1139 M:283 W: Missing Blank Line separator, <400> field identifier